

OIPE

#2

RAW SEQUENCE LISTING

DATE: 12/13/2001

PATENT APPLICATION: US/10/003,392

TIME: 09:12:54

Input Set : A:\BB1463 US NA Seq Listing.txt

Output Set: N:\CRF3\12132001\I003392.raw

ENTERED

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3 <110> APPLICANT: Allen, Stephen M.
4   Caimi, Perry G.
5   Stoop, Johan M.
7 <120> TITLE OF INVENTION: Fructan Biosynthetic Enzymes
9 <130> FILE REFERENCE: BB1463 US NA
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/003,392
C--> 12 <141> CURRENT FILING DATE: 2001-10-30
14 <150> PRIOR APPLICATION NUMBER: 60/244,273
15 <151> PRIOR FILING DATE: 2000-10-10
17 <150> PRIOR APPLICATION NUMBER: 60/269,543
18 <151> PRIOR FILING DATE: 2001-02-16
20 <160> NUMBER OF SEQ ID NOS: 21
22 <170> SOFTWARE: Microsoft Office 97
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2080
26 <212> TYPE: DNA
27 <213> ORGANISM: Dimorphotheca sinuata
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31 ttgaggacgc acccctactg aaccacaccg aaccaccacc accaccgcca ccgccaactg   120
32 ccggaagaaa acggttggtg atcaagggtg tgtcagttat caccctactc attttgctta   180
33 ttgtttcagt tttgtttctc aaccaacaaa attcaagtca ctccaccacc aattcaaaat   240
34 cgatctccca atccgatcgc ctcatTTggg aaagaacatc tttccatttt caaccgcgca   300
35 aaaatttcat ttacgatccc aatgggccaat tatttcacat ggggttggtac catcttttct   360
36 atcaatacaa cccgtacggt cctgTTTggg gaaatatgtc atgggggtcac tccgTTTcca   420
37 aagacatgat caactggttt gagcttccag tgcattggt cccaaccgaa tggtagcata   480
38 tcgagggtgt tttatccggg tccaccaccg tcttcccaa cgggtcaaac ttcgcattgt   540
39 acacaggaaa cgctaacgat ttctcccaat tacaatgcaa agctgtaccc gtcaacatat   600
40 ctgaccact tcttatcgag tgggtcaaac acgatggtaa cccaatcctg tatactccac   660
41 cagggattgg gttaaaagac tatcgggacc cgtcaacagt ctggacgggt cccgatggaa   720
42 aacatcggat gatcatggga tctaaacgaa acaaaacggg actagtactt gtttaccaca   780
43 caaccgattt cacaatttat gtgatgtcgg atgagccgtt gcattcggtta cctaataccg   840
44 atatgtggga atgcgttgac ttttaccctg tttcgttgac caatgatagc gcgcttgata   900
45 tggcggttta tgggtcgggt atcaaacacg tgattaaaga aagttgggag ggacatggaa   960
46 tggattggta ttcgattggg acttatgatg catcaaccga taaatggact ccggataacc  1020
47 cgaaattaga tgtgggtatc gggttgcgat gtgattacgg aaagtTTTTT gcacgaaga  1080
48 gtcttttcga tccgttgaag aaaaggaggg tgacttgggg ttatgttggg gaatcagata  1140
49 aacctgatca ggacctctct agaggatggg ctaccattta taatgttgca cggacggtgg  1200
50 tactagatag aaagaccgga acacatctac ttcattggcc agttgaagaa atcgagagtt  1260
51 tgagatccaa tgggtcaagaa ttcaacgaga ttgaactcaa accgggttcg atcattccac  1320
52 ttgacatagg ctcggtactc cagttggaca tagttgcgac atttgaagtg gatcaagatg  1380
53 cgttgaaagc tataagtga aaccaacgaag aatatatttg taccaaaagc tgggggtgcag  1440
54 ccggaagggg aagtttgagg ccatttgagg ttgcggtttt agccgatgga acactttcag  1500
55 agttaactcc cgtgtatttc tacatagcta aaaatacggg tggaagtgtg gcaacacatt  1560
56 tttgtaccga taagctaaga tcatcactag attatgatcg tgaaagagtg gtgtatggaa  1620
57 gcactgtccc tgtgcttgat ggtgaagaac tcacaatgag gttattggtg gaccattcgg  1680
58 tagtagaagg gtttgcgcaa ggaggaagga cggtaataac atcaagggtc tatccgacaa  1740

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59 aggcaatata cgacaacgcg aagggtgttct tattcaacaa cgctactggt acgagtgtga 1800
60 aggcgtctct caagatttgg caaatggctc ctgcccagat taaaccttac cctctttaat 1860
61 catatgtttc atttcactct cactagaaca cttgctgtta ctattattgt atcttatatt 1920
62 ttttatatgt acgtaataat taccgtttgg atggttttgt tttgttcaac ctctgcattg 1980
63 tgtgttaagt agtaagccgc gattatttta ataatatgaa taggttggtt tgttcaaaaa 2040
64 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2080
66 <210> SEQ ID NO: 2
67 <211> LENGTH: 608
68 <212> TYPE: PRT
69 <213> ORGANISM: Dimorphotheca sinuata
71 <400> SEQUENCE: 2
72 Met Thr Thr Thr Lys Pro Phe Ser Asp Leu Glu Asp Ala Pro Leu Leu
73 1 5 10 15
75 Asn His Thr Glu Pro Pro Pro Pro Pro Pro Thr Ala Gly Arg
76 20 25 30
78 Lys Arg Leu Leu Ile Lys Val Val Ser Val Ile Thr Leu Leu Ile Leu
79 35 40 45
81 Leu Ile Val Ser Val Leu Phe Leu Asn Gln Gln Asn Ser Ser His Ser
82 50 55 60
84 Thr Thr Asn Ser Lys Ser Ile Ser Gln Ser Asp Arg Leu Ile Trp Glu
85 65 70 75 80
87 Arg Thr Ser Phe His Phe Gln Pro Ala Lys Asn Phe Ile Tyr Asp Pro
88 85 90 95
90 Asn Gly Pro Leu Phe His Met Gly Trp Tyr His Leu Phe Tyr Gln Tyr
91 100 105 110
93 Asn Pro Tyr Gly Pro Val Trp Gly Asn Met Ser Trp Gly His Ser Val
94 115 120 125
96 Ser Lys Asp Met Ile Asn Trp Phe Glu Leu Pro Val Ala Leu Val Pro
97 130 135 140
99 Thr Glu Trp Tyr Asp Ile Glu Gly Val Leu Ser Gly Ser Thr Thr Val
100 145 150 155 160
102 Leu Pro Asn Gly Gln Ile Phe Ala Leu Tyr Thr Gly Asn Ala Asn Asp
103 165 170 175
105 Phe Ser Gln Leu Gln Cys Lys Ala Val Pro Val Asn Ile Ser Asp Pro
106 180 185 190
108 Leu Leu Ile Glu Trp Val Lys Tyr Asp Gly Asn Pro Ile Leu Tyr Thr
109 195 200 205
111 Pro Pro Gly Ile Gly Leu Lys Asp Tyr Arg Asp Pro Ser Thr Val Trp
112 210 215 220
114 Thr Gly Pro Asp Gly Lys His Arg Met Ile Met Gly Ser Lys Arg Asn
115 225 230 235 240
117 Lys Thr Gly Leu Val Leu Val Tyr His Thr Thr Asp Phe Thr Asn Tyr
118 245 250 255
120 Val Met Ser Asp Glu Pro Leu His Ser Val Pro Asn Thr Asp Met Trp
121 260 265 270
123 Glu Cys Val Asp Phe Tyr Pro Val Ser Leu Thr Asn Asp Ser Ala Leu
124 275 280 285
126 Asp Met Ala Ala Tyr Gly Ser Gly Ile Lys His Val Ile Lys Glu Ser
127 290 295 300

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129 Trp Glu Gly His Gly Met Asp Trp Tyr Ser Ile Gly Thr Tyr Asp Ala
130 305                      310                      315                      320
132 Ser Thr Asp Lys Trp Thr Pro Asp Asn Pro Lys Leu Asp Val Gly Ile
133                      325                      330                      335
135 Gly Leu Arg Cys Asp Tyr Gly Lys Phe Phe Ala Ser Lys Ser Leu Phe
136                      340                      345                      350
138 Asp Pro Leu Lys Lys Arg Arg Val Thr Trp Gly Tyr Val Gly Glu Ser
139                      355                      360                      365
141 Asp Lys Pro Asp Gln Asp Leu Ser Arg Gly Trp Ala Thr Ile Tyr Asn
142                      370                      375                      380
144 Val Ala Arg Thr Val Val Leu Asp Arg Lys Thr Gly Thr His Leu Leu
145 385                      390                      395                      400
147 His Trp Pro Val Glu Ile Glu Ser Leu Arg Ser Asn Gly Gln Glu
148                      405                      410                      415
150 Phe Asn Glu Ile Glu Leu Lys Pro Gly Ser Ile Ile Pro Leu Asp Ile
151                      420                      425                      430
153 Gly Ser Ala Thr Gln Leu Asp Ile Val Ala Thr Phe Glu Val Asp Gln
154                      435                      440                      445
156 Asp Ala Leu Lys Ala Ile Ser Glu Thr Asn Glu Glu Tyr Ile Cys Thr
157                      450                      455                      460
159 Lys Ser Trp Gly Ala Ala Gly Arg Gly Ser Leu Gly Pro Phe Gly Val
160 465                      470                      475                      480
162 Ala Val Leu Ala Asp Gly Thr Leu Ser Glu Leu Thr Pro Val Tyr Phe
163                      485                      490                      495
165 Tyr Ile Ala Lys Asn Thr Asp Gly Ser Val Ala Thr His Phe Cys Thr
166                      500                      505                      510
168 Asp Lys Leu Arg Ser Ser Leu Asp Tyr Asp Arg Glu Arg Val Val Tyr
169                      515                      520                      525
171 Gly Ser Thr Val Pro Val Leu Asp Gly Glu Glu Leu Thr Met Arg Leu
172                      530                      535                      540
174 Leu Val Asp His Ser Val Val Glu Gly Phe Ala Gln Gly Gly Arg Thr
175 545                      550                      555                      560
177 Val Ile Thr Ser Arg Val Tyr Pro Thr Lys Ala Ile Tyr Asp Asn Ala
178                      565                      570                      575
180 Lys Val Phe Leu Phe Asn Asn Ala Thr Gly Thr Ser Val Lys Ala Ser
181                      580                      585                      590
183 Leu Lys Ile Trp Gln Met Ala Pro Ala Gln Ile Lys Pro Tyr Pro Leu
184                      595                      600                      605

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186 <210> SEQ ID NO: 3

187 <211> LENGTH: 2146

188 <212> TYPE: DNA

189 <213> ORGANISM: Parthenium argentatum Grey

191 <400> SEQUENCE: 3

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192 gcacgaggag accagtcagc acacagtaac tgaactcact caaccatta ttcaccttca 60
193 ccatgacaac ccctgaacaa cccattacag accttgaaca cgaaccacac cacaaccgca 120
194 cacccttatt ggaccacaac gaatcacaac ccgtaaagaa acatttggtc ttcaaagtgc 180
195 tgtctggtgt taccttcatt tcattgttct ttatttctgc ttttttattc attgttttga 240
196 accaacaataa ttctaccaat atatcggtta agtactcgca atccgatcgc cttacgtggg 300
197 aacgaaccgc ttttcatttt caaccggcca agaattttat ttatgatccc aatgggtcaa 360

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198 tgtactacat gggctggtac catctattct atcaatacaa tccatacgca ccggtttggg 420
199 gtaatatgtc atggggtcac tccgtatcca aagacatgat caactggtac gagctaccg 480
200 tcgctatagt cccgactgaa tggatatgata ttgagggcgt cttatctggg tccatcacag 540
201 tgcttcccaa cgggcagatc tttgcattgt acacggggaa tgctaatac ttttcccaat 600
202 tgcaatgcaa agctgtaccc gtgaactcat ctgacccact tcttggtgag tgggtcaagt 660
203 acgaagataa cccaatcctg tacactccac cagggattgg gttaaaagac tatagggacc 720
204 cgtcaacagt ctggacgggt cctgatggaa agcataggat gatcatggga actaaacgtg 780
205 gcaatacagg aatgatactt gtttaccata ccaactgatta cacgaactat gagatggtga 840
206 atgagcctat gcaactcggt cccaataacc atatgtggga atgcgttgac ttttaccggg 900
207 tttcattaac caacgatagt gcaacttgata ttgcggccta cgggtcgggt atcaaacacg 960
208 tgattaaaga aagttgggag ggatatggga tggatttcta ttcaatcggg acttatgacg 1020
209 catttaacga taaatggact cccgataacc cagagttaga tgttggtatc gggttgcggg 1080
210 gtgattacgg taggtttttt gcatcaaaga gtatttttga cccagtgaag aaaaggagga 1140
211 tcacttgggc ttatgttgga gaatcagata atgctgatga tgacctctcc agaggatggg 1200
212 ctactattta taatgttgga agaactattg tactagatag aaagaccggg acccatttac 1260
213 ttcattggcc tgtcagaggaa atcagagagt tgagatacaa tggtcaggaa tttaaagaga 1320
214 tcaactaga gcccggttca attgctccac tcgacatagg caccgctaca cagttggaca 1380
215 tagttgcaac atttaagggt gatgaggctg cattgaacgc gacaagtga accgatgata 1440
216 acttcgcttg caccacgagc tcaggtgcag ttgaaagggg aagtttgga ccatttggtc 1500
217 ttgcggttct agctgatgga accctttccg agttaactcc ggtttatttc tacattgcta 1560
218 aaaaggccga tggaggtgtg tcaacacatt tttgtaccga taagctaagg tcatccttgg 1620
219 attttgataa ggagagagtg gtgtacggtg gcaactgttc tgtgttagat gatgaagaac 1680
220 tcacaatgag gctattggtg gatcattcgg tagtcgaggc gtttgcacaa ggaggaagga 1740
221 ttgcataaac atcaaggggtg tatccgacga aagcaatata cgaaggagcg aagttgttct 1800
222 tattcaacaa tgccacggat acgagtgtga aggcattctc caagatttg caaatggctt 1860
223 ctgccccaaat tcatcaatac gagtttaatt aggggctctc gttatcctta ttattagtat 1920
224 ttatgtattt taatttattt agacctatgt atttgatcat atgagttctt atcgtgcttt 1980
225 aagtagtaaa tgaattgtgt ttgggtaaaa aaataaaaaa aaaaaaaaaa aaaaaaaaaa 2040
226 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2100
227 gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2146
230 <210> SEQ ID NO: 4
231 <211> LENGTH: 609
232 <212> TYPE: PRT
233 <213> ORGANISM: Parthenium argentatum Grey
235 <400> SEQUENCE: 4
236 Met Thr Thr Pro Glu Gln Pro Ile Thr Asp Leu Glu His Glu Pro Asn
237 1 5 10 15
239 His Asn Arg Thr Pro Leu Leu Asp His Asn Glu Ser Gln Pro Val Lys
240 20 25 30
242 Lys His Leu Phe Phe Lys Val Leu Ser Gly Val Thr Phe Ile Ser Leu
243 35 40 45
245 Phe Phe Ile Ser Ala Phe Leu Phe Ile Val Leu Asn Gln Gln Asn Ser
246 50 55 60
248 Thr Asn Ile Ser Val Lys Tyr Ser Gln Ser Asp Arg Leu Thr Trp Glu
249 65 70 75 80
251 Arg Thr Ala Phe His Phe Gln Pro Ala Lys Asn Phe Ile Tyr Asp Pro
252 85 90 95
254 Asn Gly Gln Met Tyr Tyr Met Gly Trp Tyr His Leu Phe Tyr Gln Tyr
255 100 105 110

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257 Asn Pro Tyr Ala Pro Val Trp Gly Asn Met Ser Trp Gly His Ser Val
258      115      120      125
260 Ser Lys Asp Met Ile Asn Trp Tyr Glu Leu Pro Val Ala Ile Val Pro
261      130      135      140
263 Thr Glu Trp Tyr Asp Ile Glu Gly Val Leu Ser Gly Ser Ile Thr Val
264 145      150      155      160
266 Leu Pro Asn Gly Gln Ile Phe Ala Leu Tyr Thr Gly Asn Ala Asn Asp
267      165      170      175
269 Phe Ser Gln Leu Gln Cys Lys Ala Val Pro Val Asn Ser Ser Asp Pro
270      180      185      190
272 Leu Leu Val Glu Trp Val Lys Tyr Glu Asp Asn Pro Ile Leu Tyr Thr
273      195      200      205
275 Pro Pro Gly Ile Gly Leu Lys Asp Tyr Arg Asp Pro Ser Thr Val Trp
276      210      215      220
278 Thr Gly Pro Asp Gly Lys His Arg Met Ile Met Gly Thr Lys Arg Gly
279 225      230      235      240
281 Asn Thr Gly Met Ile Leu Val Tyr His Thr Thr Asp Tyr Thr Asn Tyr
282      245      250      255
284 Glu Met Leu Asn Glu Pro Met His Ser Val Pro Asn Thr Asp Met Trp
285      260      265      270
287 Glu Cys Val Asp Phe Tyr Pro Val Ser Leu Thr Asn Asp Ser Ala Leu
288      275      280      285
290 Asp Ile Ala Ala Tyr Gly Ser Gly Ile Lys His Val Ile Lys Glu Ser
291      290      295      300
293 Trp Glu Gly Tyr Gly Met Asp Phe Tyr Ser Ile Gly Thr Tyr Asp Ala
294 305      310      315      320
296 Phe Asn Asp Lys Trp Thr Pro Asp Asn Pro Glu Leu Asp Val Gly Ile
297      325      330      335
299 Gly Leu Arg Cys Asp Tyr Gly Arg Phe Ala Ser Lys Ser Ile Phe
300      340      345      350
302 Asp Pro Val Lys Lys Arg Arg Ile Thr Trp Ala Tyr Val Gly Glu Ser
303      355      360      365
305 Asp Asn Ala Asp Asp Asp Leu Ser Arg Gly Trp Ala Thr Ile Tyr Asn
306      370      375      380
308 Val Gly Arg Thr Ile Val Leu Asp Arg Lys Thr Gly Thr His Leu Leu
309 385      390      395      400
311 His Trp Pro Val Glu Glu Ile Glu Ser Leu Arg Tyr Asn Gly Gln Glu
312      405      410      415
314 Phe Lys Glu Ile Lys Leu Glu Pro Gly Ser Ile Ala Pro Leu Asp Ile
315      420      425      430
317 Gly Thr Ala Thr Gln Leu Asp Ile Val Ala Thr Phe Lys Val Asp Glu
318      435      440      445
320 Ala Ala Leu Asn Ala Thr Ser Glu Thr Asp Asp Asn Phe Ala Cys Thr
321      450      455      460
323 Thr Ser Ser Gly Ala Val Glu Arg Gly Ser Leu Gly Pro Phe Gly Leu
324 465      470      475      480
326 Ala Val Leu Ala Asp Gly Thr Leu Ser Glu Leu Thr Pro Val Tyr Phe
327      485      490      495
329 Tyr Ile Ala Lys Lys Ala Asp Gly Gly Val Ser Thr His Phe Cys Thr

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date